

## SEQUENCE LISTING

SEQ ID NO: 1 provides a primate MIP-3 $\alpha$  polynucleotide sequence.  
SEQ ID NO: 2 provides a primate MIP-3 $\alpha$  polypeptide sequence.  
SEQ ID NO: 3 provides a murine MIP-3 $\alpha$  polynucleotide sequence.  
SEQ ID NO: 4 provides a murine (mouse) MIP-3 $\alpha$  polypeptide sequence.  
SEQ ID NO: 5 provides a murine MIP-3 $\alpha$  polynucleotide sequence.  
SEQ ID NO: 6 provides a murine (rat) MIP-3 $\alpha$  polypeptide sequence.  
SEQ ID NO: 7 provides a primate CCR6 polynucleotide sequence.  
SEQ ID NO: 8 provides a primate CCR6 polypeptide sequence.

<110> Oldham, Elizabeth R.

Homey, Bernhard

Dieu-Nosjean, Marie Caroline

Caux, Christophe

Zlotnik, Albert

<120> Chemokine Uses; Compositions; Methods

<130> DX0934K1B US

<150> US 09/503,219

<151> 2000-02-02

<150> US 60/118,335

<151> 1999-02-03

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 291

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(288)

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<222> (79)..()

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cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc	96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
-10 -5 -1 1 5	
tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc	144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
10 15 20	
ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc	192
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	
25 30 35	
ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act	240
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr	
40 45 50	
tgg gtg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg	288
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met	
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taa	291

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<212> PRT

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Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys  
-10 -5 -1 1 5

Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly  
10 15 20

Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile  
25 30 35

Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr  
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Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met  
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-25 -20 -15	

ctg ctg gct cac ctc tgc agc cag gca gaa gca agc aac tac gac tgt	96
Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ser Asn Tyr Asp Cys	
-10 -5 -1 1 5	

tgc ctc tgc tac ata cag acg cca ctt cct tcc aga gct att gtg ggt	144
Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val Gly	
10 15 20	

ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc atc	192
Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile	
25 30 35	

ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag aac	240
Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln Asn	
40 45 50	

tgg gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag atg	288
Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys Met	
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taa	291
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Met Ala Cys Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val
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Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val Gly  
                   10                  15                  20

Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile  
                   25                  30                  35

Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln Asn  
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<211> 291

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gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc	96
Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys	
-5                  -1 1                  5	

ctc acg tac aca aag aac gtg tat cat cat gcg aga aat ttt gtg ggt 144  
 Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly  
           10                  15                  20

ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct atc atc 192  
 Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile  
           25                  30                  35

ttt cac ctg aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc 240  
 Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile  
           40                  45                  50                  55

tggtgtg aaa agg att ttg cac ctc ctc agc cta aga acc aag aag atg 288  
 Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met  
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taa 291

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<213> Rattus sp.

<400> 6

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Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys  
                   -5                  -1 1                  5

Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly  
           10                  15                  20

Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile  
           25                  30                  35

Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile  
           40                  45                  50                  55

Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met  
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<210> 7

<211> 1098

<212> DNA

<213> Homo sapiens

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<223> n may be a, c, g, or t

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Met	Phe	Ser	Thr	Pro	Val	Lys	Ile	Ile	Leu	Cys	Gln	Ser	Ile	Leu	His	
1				5					10					15		

att	act	cag	ttg	att	ctg	aga	tgt	tac	tgt	gct	cct	tgc	agg	agg	tca	96
Ile	Thr	Gln	Leu	Ile	Leu	Arg	Cys	Tyr	Cys	Ala	Pro	Cys	Arg	Arg	Ser	
			20					25					30			

ggc	agt	tct	cca	ggc	tat	ttg	tac	cga	att	gcc	tac	tcc	ttg	atc	tgt	144
Gly	Ser	Ser	Pro	Gly	Tyr	Leu	Tyr	Arg	Ile	Ala	Tyr	Ser	Leu	Ile	Cys	
			35				40					45				

gtt	ctt	ggc	ctc	ctg	ggg	aat	att	ctg	gtg	gtg	atc	acc	ttt	gct	ttt	192
Val	Leu	Gly	Leu	Leu	Gly	Asn	Ile	Leu	Val	Val	Ile	Thr	Phe	Ala	Phe	
			50				55				60					

tat	aag	aag	gcc	agg	tct	atg	aca	gac	gtc	tat	ctc	ttg	aac	atg	gcc	240
Tyr	Lys	Lys	Ala	Arg	Ser	Met	Thr	Asp	Val	Tyr	Leu	Leu	Asn	Met	Ala	
65					70					75					80	

att	gca	gac	atc	ctc	ttt	gtt	ctt	act	ctc	cca	ttc	tgg	gca	gtg	agt	288
Ile	Ala	Asp	Ile	Leu	Phe	Val	Leu	Thr	Leu	Pro	Phe	Trp	Ala	Val	Ser	
				85					90					95		

cat	gcc	act	ggt	gcg	tgg	gtt	ttc	agc	aat	gcc	acg	tgc	aag	ttg	cta	336
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His	Ala	Thr	Gly	Ala	Trp	Val	Phe	Ser	Asn	Ala	Thr	Cys	Lys	Leu	Leu		
			100					105					110				
aaa	ggc	atc	tat	gcc	atc	aac	ttt	aac	tgc	ggg	atg	ctg	ctc	ctg	act	384	
Lys	Gly	Ile	Tyr	Ala	Ile	Asn	Phe	Asn	Cys	Gly	Met	Leu	Leu	Leu	Thr		
			115				120					125					
tgc	att	agc	atg	gac	cgg	tac	atc	gcc	att	gta	cag	gcg	act	aag	tca	432	
Cys	Ile	Ser	Met	Asp	Arg	Tyr	Ile	Ala	Ile	Val	Gln	Ala	Thr	Lys	Ser		
			130				135				140						
ttc	cgg	ctc	cga	tcc	aga	aca	cta	ccg	cgc	agc	aaa	atc	atc	tgc	ctt	480	
Phe	Arg	Leu	Arg	Ser	Arg	Thr	Leu	Pro	Arg	Ser	Lys	Ile	Ile	Cys	Leu		
							145				155				160		
gtt	gtg	tgg	ggg	ctg	tca	gtc	atc	atc	tcc	agc	tca	act	ttt	gtc	ttc	528	
Val	Val	Trp	Gly	Leu	Ser	Val	Ile	Ile	Ser	Ser	Ser	Thr	Phe	Val	Phe		
							165				170				175		
aac	caa	aaa	tac	aac	acc	caa	ggc	agc	gat	gtc	tgt	gaa	ccc	aag	tac	576	
Asn	Gln	Lys	Tyr	Asn	Thr	Gln	Gly	Ser	Asp	Val	Cys	Glu	Pro	Lys	Tyr		
							180				185			190			
can	act	gtc	tgc	gag	ccc	atc	agg	tgg	aag	ctg	ctg	atg	ttg	ggg	ctt	624	
Thr	Thr	Val	Ser	Glu	Pro	Ile	Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu		
							195					205					
gag	cta	ctc	ttt	ggt	ttc	ttt	atc	cct	ttg	atg	ttc	atg	ata	ttt	tgt	672	
Glu	Leu	Leu	Phe	Gly	Phe	Phe	Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys		
							210					220					
tac	acg	ttc	att	gtc	aaa	acc	ttg	gtg	caa	gct	cag	aat	tct	aaa	agg	720	
Tyr	Thr	Phe	Ile	Val	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg		
							225				235				240		
cac	aaa	gcc	atc	cgt	gta	atc	ata	gct	gtg	gtg	ctt	gtg	ttt	ctg	gct	768	
His	Lys	Ala	Ile	Arg	Val	Ile	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala		
							245				250				255		
tgt	cag	att	cct	cat	aac	atg	gtc	ctg	ctt	gtg	acg	gct	gct	aat	ttg	816	
Cys	Gln	Ile	Pro	His	Asn	Met	Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu		
							260					270					
ggt	aaa	atg	aac	cga	tcc	tgc	cag	agc	gaa	aag	cta	att	ggc	tat	acg	864	
Gly	Lys	Met	Asn	Arg	Ser	Cys	Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr		
							275					285					
aaa	act	gtc	aca	gaa	gtc	ctg	gct	ttc	ctg	cac	tgc	tgc	ctg	aac	cct	912	
Lys	Thr	Val	Thr	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro		
							290				300						
gtg	ctc	tac	gct	ttt	att	ggg	cag	aag	ttc	aga	aac	tac	ttt	ctg	aag	960	
Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys		
							305				315				320		
atc	ttg	aag	gac	ctg	tgg	tgt	gtg	aga	agg	aag	tac	aag	tcc	tca	ggc	1008	



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Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly
      325                      330                      335

ttc tcc tgt gcc ggg agg tac tca gaa aac att tct cgg cag acc agt      1056
Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser
      340                      345                      350

gag acc gca gat aac gac aat gcg tcg tcc ttc act atg tga      1098
Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met
      355                      360                      365

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<211> 365

<212> PRT

<213> Homo sapiens

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<222> (579)..(579)

<223> n may be a, c, g, or t

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Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
      35                      40                      45

Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
      50                      55                      60

Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
65                      70                      75                      80

Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser
      85                      90                      95

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His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu  
 100 105 110

Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr  
 115 120 125

Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser  
 130 135 140

Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu  
 145 150 155 160

Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe  
 165 170 175

Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr  
 180 185 190

Thr Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu  
 195 200 205

Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys  
 210 215 220

Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg  
 225 230 235 240

His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala  
 245 250 255

Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu  
 260 265 270

Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr  
 275 280 285

Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro  
 290 295 300

Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys  
 305 310 315 320

Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly  
325 330 335

Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser  
340 345 350

Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met  
355 360 365